

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

Display Show:

☐ 1: XP_153478. hypothetical prot...[gi:20909630]

[BLink](#), [Links](#)

LOCUS LOC217730 197 aa linear ROD 17-MAY-2002
 DEFINITION hypothetical protein XP_153478 [Mus musculus].
 ACCESSION XP_153478
 VERSION XP_153478.1 GI:20909630
 DBSOURCE REFSEQ: accession XM_153478.1
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 197)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was
 predicted from NCBI contig NW_000053 by automated computational
 analysis using gene prediction method: GenomeScan.
 Also see:
 [Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..197 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /chromosome="12"
<u>Protein</u>	1..197 /product="hypothetical protein XP_153478"
<u>CDS</u>	1..197 /gene="LOC217730" /coded_by="XM_153478.1:1..594" /db_xref="InterimID:217730"

ORIGIN


```

1 metasaapr vwpfhfafla gflshpeths pgepgplprp pacpsvpfmw vaqwirlifv
61 tldvlgsqpm kcpghvalhq dpgpvvrpsg shgnalpldc lmgptshwnv skippfrqps
121 kppltdgssq fqqgenpfra cpdfqlgkqm atiakarhnp syilfphpsl snsnavvtln
181 rqnlsdssv sissqss
//

```

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12

 **NCBI** *protein-protein* **BLAST**

Nucleotide Protein Translations Retrieve results for an RID

Search

pykwpfhfaffhqilatstiamshcrptvykqtsii
pykwpfhfaffhqilatstiamshcrptvykqtsii

Set
subsequence

From: To:

Choose
database

nr

Do CD-Search

☐

Now:

BLAST!

or

Reset query

Reset all

Options for advanced blasting

Limit by entrez
query

or select from:

(none)

Composition-based
statistics

☐

Choose filter

☐

Low complexity

☐

Mask for lookup table only

☐

Mask lower case

Expect

20000

Word Size

2

Matrix

PAM30

Gap Costs

Existence: 9 Extension: 1

PSSM

Other advanced

PHI pattern



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books	
Search		Protein	for					Go	Clear
		Limits	Preview/Index	History	Clipboard		Details		
Display	default	Show:	20	Send to	File	Get Subsequence			

☐ 1: XP_153478. hypothetical prot...[gi:20909630]

[BLink](#), [Links](#)

LOCUS LOC217730 197 aa linear ROD 17-MAY-2002
 DEFINITION hypothetical protein XP_153478 [Mus musculus].
 ACCESSION XP_153478
 VERSION XP_153478.1 GI:20909630
 DBSOURCE REFSEQ: accession XM_153478.1
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 197)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was
 predicted from NCBI contig NW_000053 by automated computational
 analysis using gene prediction method: GenomeScan.
 Also see:
[Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..197 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /chromosome="12"
<u>Protein</u>	1..197 /product="hypothetical protein XP_153478"
<u>CDS</u>	1..197 /gene="LOC217730" /coded_by="XM_153478.1:1..594" /db_xref="InterimID:217730"

ORIGIN
 1 metasaaprr vwpfhfafla gflshpeths pgepgplprp pacpsvpfmw vaqwirlifv
 61 tldvlgspqm kcpghvalhq dpgpvvrpsg shgnalpldc lmgptshwnv skippfrqps
 121 kppltdgssq fqqgenpfra cpdfqlgkqm atiakarhpp sylfphpsl snsnavvtln
 181 rqnlsdssv sissqss
 //

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12



results of BLAST

search 1

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053456915-026125-1387

Query=

(34 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

No significant similarity found. For reasons why, [click here](#).

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

Posted date: May 20, 2003 1:52 AM

Number of letters in database: 461,393,641

Number of sequences in database: 1,435,412

Lambda	K	H
0.335	0.141	0.505

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 28,353,653

Number of Sequences: 1435412

Number of extensions: 452865

Number of successful extensions: 1347

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 1347

Number of HSP's gapped (non-prelim): 0

length of query: 34

length of database: 461,393,641

effective HSP length: 10

effective length of query: 24

effective length of database: 447,039,521

effective search space: 10728948504

effective search space used: 10728948504

T: 11

A: 40

X1: 15 (7.3 bits)

X2: 38 (14.6 bits)

**results of BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053457733-016164-25584

Query=

(36 letters)

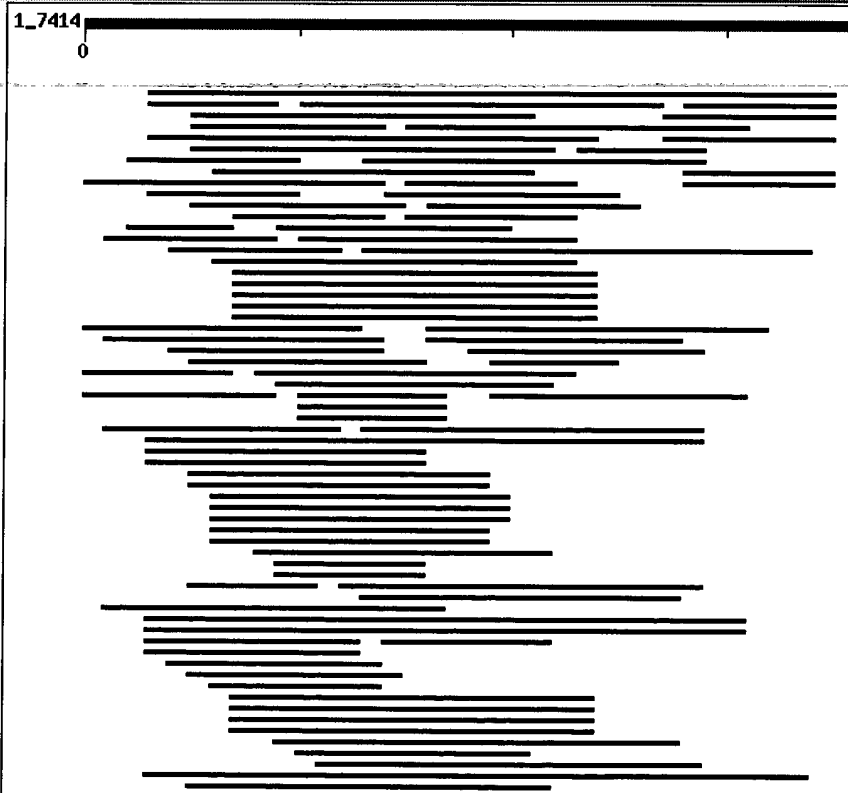
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 21287767 gb EAA00088.1	ENSANGP00000017962 [Anopheles ga...	31	1.6	
gi 20909630 ref XP_153478.1	hypothetical protein XP_153478...	30	3.8	L
gi 27695175 ref XP_223369.1	similar to low density lipopro...	28	12	L
gi 21242454 ref NP_642036.1	MFS transporter [Xanthomonas a...	28	12	
gi 28900823 ref NP_800478.1	3-hydroxy-3-methylglutaryl CoA...	28	16	
gi 30177923 gb EAA45104.1	ENSANGP00000023294 [Anopheles ga...	28	16	
gi 21231138 ref NP_637055.1	MFS transporter [Xanthomonas c...	28	16	
gi 23137395 ref ZP_00119101.1	hypothetical protein [Cytoph...	27	22	
gi 21245069 ref NP_644651.1	conserved hypothetical protein...	27	22	
gi 24374681 ref NP_718724.1	DnaJ domain protein [Shewanell...	27	30	
gi 18398283 ref NP_565400.1	F-box protein family, AtFBL10 ...	27	30	
gi 10946860 ref NP_067441.1	TATA box binding protein (Tbp)...	27	30	L
gi 18462766 gb AAL72538.1	hypothetical protein [Shigella f...	27	30	
gi 27672343 ref XP_221755.1	similar to hypothetical protei...	27	30	L
gi 28871387 ref NP_794006.1	hypothetical protein [Pseudomo...	27	30	
gi 23128861 ref ZP_00110699.1	hypothetical protein [Nostoc...	27	30	
gi 21293138 gb EAA05283.1	ENSANGP00000008298 [Anopheles ga...	27	40	
gi 9801567 gb AAF97943.2	cytochrome P450 CYP6N4v3 [Aedes a...	27	40	
gi 9801568 gb AAF97944.2	cytochrome P450 CYP6N4v4 [Aedes a...	27	40	
gi 9801569 gb AAF97945.2	cytochrome P450 CYP6N4v5 [Aedes a...	27	40	
gi 28564982 gb AAO38684.1	truncated PDR5 [Saccharomyces kl...	27	40	
gi 15078968 ref NP_149719.1	256R [Invertebrate iridescent ...	27	40	
gi 15641102 ref NP_230734.1	periplasmic binding protein-re...	27	40	
gi 19114288 ref NP_593376.1	hypothetical protein [Schizosa...	27	40	
gi 9801570 gb AAF97946.2	cytochrome P450 CYP6N4v6 [Aedes a...	27	40	
gi 9801564 gb AAF97940.2	cytochrome P450 CYP6N4v1 [Aedes a...	27	40	
gi 729930 sp P16270 LECN_PEA	NONSEED LECTIN PRECURSOR >gi 3...	26	53	
gi 30260580 ref NP_842957.1	hypothetical protein [Bacillus...	26	53	
gi 22293495 emb CAD31853.1	putative chemosensory receptor ...	26	53	
gi 26987557 ref NP_742982.1	conserved hypothetical protein...	26	53	
gi 30023459 ref NP_835090.1	Beta-1,3-N-acetylglucosaminylt...	26	53	
gi 17230565 ref NP_487113.1	probable glycosyl transferase ...	26	53	
gi 27500354 ref XP_211309.1	hypothetical protein XP_211309...	26	53	L
gi 13812138 ref NP_113265.1	chromosomal region maintenance...	26	53	
gi 27706584 ref XP_242294.1	hypothetical protein XP_242294...	26	53	L
gi 100052 pir S20988	lectin - garden pea >gi 169172 gb AAA...	26	53	
gi 7510844 pir T29765	hypothetical protein ZC581.4 - Caeno...	26	53	
gi 21398366 ref NP_654351.1	hypothetical protein predicted...	26	53	
gi 5579428 gb AAD45549.1 U70376_14	SpCE [Streptomyces netro...	26	53	
gi 630666 pir S40748	hypothetical protein F54C8.6 - Caenor...	26	72	
gi 28917410 gb EAA27114.1	hypothetical protein [Neurospora...	26	72	
gi 23612355 ref NP_703935.1	transportin [Plasmodium falcip...	26	72	
gi 15802965 ref NP_288995.1	Z3699 gene product [Escherichi...	26	72	
gi 16130359 ref NP_416929.1	orf, hypothetical protein [Esc...	26	72	
gi 17297993 dbj BAB78507.1	transportin [Plasmodium falcipa...	26	72	
gi 19113394 ref NP_596602.1	SNF2 family dna repair protein...	26	72	
gi 13476001 ref NP_107571.1	ABC transporter, substrate bin...	26	72	
gi 30020491 ref NP_832122.1	hypothetical protein [Bacillus...	26	72	
gi 22298512 ref NP_681759.1	ORF_ID:tlr0969-probable membra...	26	72	
gi 21292670 gb EAA04815.1	ENSANGP00000019532 [Anopheles ga...	26	72	
gi 23059042 ref ZP_00084044.1	hypothetical protein [Pseudo...	26	72	
gi 15964592 ref NP_384945.1	PROBABLE RIBONUCLEASE HII PROT...	26	72	
gi 28901509 ref NP_801164.1	putative ferrichrome ABC trans...	26	72	
gi 17553568 ref NP_499077.1	Predicted CDS, putative membra...	26	72	L
gi 15240890 ref NP_195730.1	expressed protein [Arabidopsis...	26	72	
gi 15889786 ref NP_355467.1	AGR_C_4580p [Agrobacterium tum...	26	72	
gi 23307111 dbj BAC16541.1	ferric vibrioferrin transport s...	26	72	
gi 30176975 gb EAA08960.2	ENSANGP00000019639 [Anopheles ga...	26	72	
gi 18860525 ref NP_573365.1	CG7876-PA [Drosophila melanoga...	26	72	L
gi 27753111 emb CAA84735.2	C. elegans SRG-11 protein (corr...	26	72	

gi 25342678 pir B88555	protein F54C8.6 [imported] - Caenor...	26	72	
gi 30157001 ref XP_291865.2	similar to olfactory receptor ...	25	96	L
gi 27707330 ref XP_242328.1	hypothetical protein XP_242328...	25	96	L
gi 15611696 ref NP_223347.1	putative TYPE II DNA MODIFICAT...	25	96	
gi 15217347 gb AAK92685.1 AC090714.18	putative retrotranspo...	25	96	
gi 630612 pir S44629	F22B7.10 protein - Caenorhabditis ele...	25	96	
gi 16944534 emb CAD11330.1	hypothetical protein [Neurospor...	25	96	
gi 30179202 gb EAA45649.1	ENSANGP00000024832 [Anopheles ga...	25	96	
gi 27685447 ref XP_217453.1	serine (or cysteine) proteinas...	25	96	L
gi 1477386 gb AAC37338.1	This CDS feature is included to s...	25	96	
gi 24666563 ref NP_649079.2	CG6836-PA [Drosophila melanoga...	25	96	L
gi 17861760 gb AAL39357.1	GH26215p [Drosophila melanogaster]	25	96	L
gi 121111 sp P07092 GDN_RAT	Glia derived nexin precursor (G...	25	96	L
gi 30179203 gb EAA45650.1	ENSANGP00000025224 [Anopheles ga...	25	96	
gi 15232200 ref NP_186830.1	expressed protein [Arabidopsis...	25	96	
gi 13660729 gb AAK32960.1	cytochrome P450 [Anopheles gambiae]	25	96	
gi 28515296 ref XP_288452.1	hypothetical protein XP_288452...	25	96	L
gi 26336525 dbj BAC31945.1	unnamed protein product [Mus mu...	25	96	L
gi 30840221 emb CAD61285.1	fertility restorer [Raphanus sa...	25	96	
gi 17552842 ref NP_498909.1	Dumpy : shorter than wild-type...	25	96	L
gi 30179201 gb EAA45648.1	ENSANGP00000025060 [Anopheles ga...	25	96	
gi 20837204 ref XP_158536.1	hypothetical protein XP_158536...	25	129	L
gi 29349732 ref NP_813235.1	conserved hypothetical protein...	25	129	
gi 15131119 emb CAC48190.1	NADH dehydrogenase subunit 2 [L...	25	129	
gi 23273294 gb AAH34950.1	TANK-binding kinase 1 [Homo sapi...	25	129	L
gi 7019547 ref NP_037386.1	TANK-binding kinase 1; NF-kB-ac...	25	129	L
gi 23058842 ref ZP_00083865.1	hypothetical protein [Pseudo...	25	129	
gi 26991318 ref NP_746743.1	conserved hypothetical protein...	25	129	
gi 23042124 ref ZP_00073532.1	hypothetical protein [Tricho...	25	129	
gi 15791673 ref NP_281496.1	hypothetical protein Cj0305c [...	25	129	
gi 26655514 gb AAN85858.1	NADH dehydrogenase subunit II [M...	25	129	
gi 14276199 gb AAK58140.1	NADH dehydrogenase subunit II [M...	25	129	
gi 14276231 gb AAK58156.1	NADH dehydrogenase subunit II [B...	25	129	
gi 22957373 gb ZP_00005078.1	hypothetical protein [Rhodoba...	25	129	
gi 17543364 ref NP_501353.1	Putative nuclear protein, with...	25	129	L
gi 15601658 ref NP_233289.1	permease [Vibrio cholerae] >gi...	25	129	
gi 27718495 ref XP_216902.1	similar to TANK-binding kinase...	25	129	L
gi 21347201 gb AAL50224.1	NADH dehydrogenase subunit II [M...	24	173	
gi 15800733 ref NP_286747.1	unknown [Escherichia coli O157...	24	173	
gi 17456139 ref XP_051362.2	similar to Transmembrane 6 sup...	24	173	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|21287767|gb|EAA00088.1| ENSANGP00000017962 [Anopheles gambiae str. PEST]
Length = 314

Score = 31.2 bits (66), Expect = 1.6

Identities = 19/47 (40%), Positives = 23/47 (48%), Gaps = 18/47 (38%)

Query: 4 WPFHFAFFH----Q-----ILATSTI--AMSHCRPTVYKQTSII 36

WP+H A FH Q IL +TI A SHC VY Q+ +I

Sbjct: 52 WPHVALFHRKDAQYFYACGGSILDENTILTA-SHC---VYTQSGVI 94

☐ >gi|20909630|ref|XP_153478.1| hypothetical protein XP_153478 [Mus musculus]
Length = 197

Score = 29.9 bits (63), Expect = 3.8

Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 4 WPFHFHAF 10
 WPFHFHAF
 Sbjct: 12 WPFHFHAF 18

☐ >gi|27695175|ref|XP_223369.1| similar to low density lipoprotein receptor-relat
 low density lipoprotein-related protein 4; Low Density
 Lipoprotein Receptor Related Protein 4; corin [Mus
 musculus] [Rattus norvegicus]
 Length = 276

Score = 28.2 bits (59), Expect = 12
 Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 6 FHFAFFHQIL 15
 FHF+ FHQ+L
 Sbjct: 2 FHFSLFHQVL 11

☐ >gi|21242454|ref|NP_642036.1| MFS transporter [Xanthomonas axonopodis pv. citri
 gi|21107899|gb|AAM36572.1| MFS transporter [Xanthomonas axonopodis pv. citri str.
 Length = 474

Score = 28.2 bits (59), Expect = 12
 Identities = 10/17 (58%), Positives = 12/17 (70%)

Query: 6 FHFAFFHQILATSTIAM 22
 F FAFF Q LA T+A+
 Sbjct: 167 FAFAFFVQFLAVPTVAL 183

☐ >gi|28900823|ref|NP_800478.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio p
 RIMD 2210633]
 gi|28809269|dbj|BAC62311.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio para
 Length = 420

Score = 27.8 bits (58), Expect = 16
 Identities = 10/18 (55%), Positives = 11/18 (61%), Gaps = 5/18 (27%)

Query: 11 FHQILATSTIAMSHCRPT 28
 FH ILATS I +PT
 Sbjct: 225 FHHILATSPI-----KPT 237

☐ >gi|30177923|gb|EAA45104.1| ENSANGP00000023294 [Anopheles gambiae str. PEST]
 Length = 232

Score = 27.8 bits (58), Expect = 16
 Identities = 15/36 (41%), Positives = 17/36 (47%), Gaps = 15/36 (41%)

Query: 4 WPFHFHAFHQ-----ILATSTI--AMSHC 25
 WP+H A FHQ IL +TI A SHC
 Sbjct: 1 WPWHAAIFHQDKHKEYACGGSILDETTILTA-SHC 35

☐ >gi|21231138|ref|NP_637055.1| MFS transporter [Xanthomonas campestris pv. campes
 33913]
 gi|21112775|gb|AAM40979.1| MFS transporter [Xanthomonas campestris pv. campestris
 33913]
 Length = 468

Score = 27.8 bits (58), Expect = 16
 Identities = 10/18 (55%), Positives = 13/18 (72%)

Query: 6 FHFAFFHQILATSTIAMS 23
 F FAFF Q LA ++A+S
 Sbjct: 166 FAFAFFLQFLAVPSVALS 183

☐ >gi|23137395|ref|ZP_00119101.1| hypothetical protein [Cytophaga hutchinsonii]
Length = 414

Score = 27.4 bits (57), Expect = 22
Identities = 13/35 (37%), Positives = 16/35 (45%), Gaps = 19/35 (54%)

Query: 7 HF---AFF-----HQIL-----ATSTIAM 22
HF AFF H++L +TSTIAM
Sbjct: 264 HPVIGAFFGAMLLSHELLGKENFHIVEKSTSTIAM 298

☐ >gi|21245069|ref|NP_644651.1| conserved hypothetical protein [Xanthomonas axonop
str. 306]
gi|21110802|gb|AAM39187.1| conserved hypothetical protein [Xanthomonas axonopodis
str. 306]
Length = 129

Score = 27.4 bits (57), Expect = 22
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 3 KWPFHFAFF 11
KW F FFAFF
Sbjct: 12 KWQFRFAFF 20

☐ >gi|24374681|ref|NP_718724.1| DnaJ domain protein [Shewanella oneidensis MR-1]
gi|24349326|gb|AAN56168.1|AE015754.2 DnaJ domain protein [Shewanella oneidensis M
Length = 402

Score = 26.9 bits (56), Expect = 30
Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 6 FHFAFFHQILA 16
FH AFF QILA
Sbjct: 170 FH-AFFEQILA 179

☐ >gi|18398283|ref|NP_565400.1| F-box protein family, AtFBL10 [Arabidopsis thaliana
gi|25372906|pir|B84547 hypothetical protein At2g17020 [imported] - Arabidopsis t
gi|13605809|gb|AAK32890.1|AF367303.1 At2g17020 [Arabidopsis thaliana]
gi|22137200|gb|AAM91445.1| At2g17020/At2g17020 [Arabidopsis thaliana]
Length = 656

Score = 26.9 bits (56), Expect = 30
Identities = 9/14 (64%), Positives = 12/14 (85%), Gaps = 1/14 (7%)

Query: 11 FHQILATSTIAMSH 24
FH ILAT T+++SH
Sbjct: 370 FHDILAT-TLSLSH 382

☐ >gi|10946860|ref|NP_067441.1| TATA box binding protein (Tbp)-associated factor,
A [Mus musculus]
gi|1842204|emb|CAA71091.1| TAFI48 protein [Mus musculus]
Length = 453

Score = 26.9 bits (56), Expect = 30
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFAFF 11
WP FHF+FF
Sbjct: 380 WPAFHFSFF 388

☐ >gi|18462766|gb|AAL72538.1| hypothetical protein [Shigella flexneri 2a]
Length = 139

Score = 26.9 bits (56), Expect = 30

Identities = 11/17 (64%), Positives = 13/17 (76%), Gaps = 2/17 (11%)

Query: 14 ILATSTIAMSHCRPTVY 30
ILA+S I+M H R TVY
Sbjct: 87 ILASSKISMLH-R-TVY 101

☐ >[gi|27672343|ref|XP_221755.1|](#) similar to hypothetical protein MGC2408 [Homo sap
norvegicus]
Length = 256

Score = 26.9 bits (56), Expect = 30
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 1 PYKWPF-HFAFFHQIL 15
PY+W F FAFHH +L
Sbjct: 130 PYEW-FGDFAFHHALL 144

☐ >[gi|28871387|ref|NP_794006.1|](#) hypothetical protein [Pseudomonas syringae pv. tom
[gi|28854638|gb|AA057701.1|](#) hypothetical protein [Pseudomonas syringae pv. tomato]
Length = 1111

Score = 26.9 bits (56), Expect = 30
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 FAFHHQIL 15
FAFHHQ+L
Sbjct: 728 FAFHHQLL 735

☐ >[gi|23128861|ref|ZP_00110699.1|](#) hypothetical protein [Nostoc punctiforme]
Length = 2181

Score = 26.9 bits (56), Expect = 30
Identities = 8/12 (66%), Positives = 8/12 (66%)

Query: 10 FFHQILATSTIA 21
FFH I A TIA
Sbjct: 595 FFHHIFANPTIA 606

☐ >[gi|21293138|gb|EAA05283.1|](#) ENSANGP00000008298 [Anopheles gambiae str. PEST]
Length = 602

Score = 26.5 bits (55), Expect = 40
Identities = 8/12 (66%), Positives = 9/12 (75%)

Query: 15 LATSTIAMSHCR 26
L TSTI + HCR
Sbjct: 580 LVTSTIVLEHCR 591

☐ >[gi|9801567|gb|AAF97943.2|](#) cytochrome P450 CYP6N4v3 [Aedes albopictus]
Length = 216

Score = 26.5 bits (55), Expect = 40
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFHHQILA---TSTIAMSHC 25
F FF LA TS+ AMS+C
Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >[gi|9801568|gb|AAF97944.2|](#) cytochrome P450 CYP6N4v4 [Aedes albopictus]
Length = 216

Score = 26.5 bits (55), Expect = 40
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25
 F FF LA TS+ AMS+C
 Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >gi|9801569|gb|AAF97945.2| cytochrome P450 CYP6N4v5 [Aedes albopictus]
 Length = 216

Score = 26.5 bits (55), Expect = 40
 Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25
 F FF LA TS+ AMS+C
 Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >gi|28564982|gb|AAO38684.1| truncated PDR5 [Saccharomyces kluyveri]
 Length = 1023

Score = 26.5 bits (55), Expect = 40
 Identities = 12/20 (60%), Positives = 13/20 (65%), Gaps = 4/20 (20%)

Query: 7 HFAFFHQILA--TSTIAMSH 24
 HF FF+ L TST AMSH
 Sbjct: 639 HF-FFY-FLVSVTSTFAMSH 656

☐ >gi|15078968|ref|NP_149719.1| 256R [Invertebrate iridescent virus 6]
 gi|15042337|gb|AAK82117.1|AF303741 256R [Chilo iridescent virus]
 Length = 78

Score = 26.5 bits (55), Expect = 40
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 YKWPFHF 10
 ++W FHF
 Sbjct: 39 FRWSFHF 47

☐ >gi|15641102|ref|NP_230734.1| periplasmic binding protein-related protein [Vibri
 gi|11345643|pir|A82245 periplasmic binding protein-related protein VC1089 [impor
 Vibrio cholerae (strain N16961 serogroup O1)
 gi|9655557|gb|AAF94248.1| periplasmic binding protein-related protein [Vibrio cho
 Length = 270

Score = 26.5 bits (55), Expect = 40
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 5 PFHF 13
 P+H+ FFHQ
 Sbjct: 80 PYHYTFFHQ 88

☐ >gi|19114288|ref|NP_593376.1| hypothetical protein [Schizosaccharomyces pombe]
 gi|3219957|sp|P87136|YDM5 SCHPO Hypothetical protein C57A7.05 in chromosome I
 gi|7491179|pir|T38949 hypothetical protein SPAC57A7.05 - fission yeast
 (Schizosaccharomyces pombe)
 gi|2104440|emb|CAB08763.1| hypothetical protein; similar to S. cerevisiae YDL231C
 contains 11 predicted transmembrane helices;
 leucine-serine rich [Schizosaccharomyces pombe]
 Length = 1337

Score = 26.5 bits (55), Expect = 40
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 3 KWPFHF 8
 KWPFHF
 Sbjct: 1308 KWPFHF 1313

☐ >gi|9801570|gb|AAF97946.2| cytochrome P450 CYP6N4v6 [*Aedes albopictus*]
Length = 216

Score = 26.5 bits (55), Expect = 40
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25
F FF LA TS+ AMS+C
Sbjct: 17 FVFF---LAGFETSSTAMSYC 34

☐ >gi|9801564|gb|AAF97940.2| cytochrome P450 CYP6N4v1 [*Aedes albopictus*]
Length = 435

Score = 26.5 bits (55), Expect = 40
Identities = 11/21 (52%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query: 8 FAFFHQILA---TSTIAMSHC 25
F FF LA TS+ AMS+C
Sbjct: 299 FVFF---LAGFETSSTAMSYC 316

☐ >gi|729930|sp|P16270|LECN_PEA NONSEED LECTIN PRECURSOR
gi|309675|gb|AAA33675.1| lectin
Length = 265

Score = 26.1 bits (54), Expect = 53
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 16 ATSTIAMSH 24
ATSTIA+SH
Sbjct: 235 ATSTIAVSH 243

☐ >gi|30260580|ref|NP_842957.1| hypothetical protein [*Bacillus anthracis* str. Ames]
gi|30253948|gb|AAP24443.1| hypothetical protein [*Bacillus anthracis* str. Ames]
Length = 920

Score = 26.1 bits (54), Expect = 53
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18
FHQI+ATS
Sbjct: 439 FHQIMATS 446

☐ >gi|22293495|emb|CAD31853.1| putative chemosensory receptor 7 [*Heliothis viresce*]
Length = 397

Score = 26.1 bits (54), Expect = 53
Identities = 10/17 (58%), Positives = 11/17 (64%), Gaps = 5/17 (29%)

Query: 1 PY--K-WPFHFAFFHQI 14
PY K WPF A+ HQI
Sbjct: 174 PYELKYWPF--AYIHQI 188

☐ >gi|26987557|ref|NP_742982.1| conserved hypothetical protein [*Pseudomonas putida*]
gi|24982231|gb|AAN66446.1|AE016274_3 conserved hypothetical protein [*Pseudomonas*]
Length = 136

Score = 26.1 bits (54), Expect = 53
Identities = 12/30 (40%), Positives = 14/30 (46%), Gaps = 15/30 (50%)

Query: 16 ATSTIAMSHC-----RPTVYKQ 32
A+ST+AMS C R VYKQ
Sbjct: 42 ASSTVAMSACIGAETQVQDQRLNR--VYKQ 69

☐ >gi|30023459|ref|NP_835090.1| Beta-1,3-N-acetylglucosaminyltransferase [Bacillus
14579]
gi|29899020|gb|AAP12291.1| Beta-1,3-N-acetylglucosaminyltransferase [Bacillus cer
14579]
Length = 326

Score = 26.1 bits (54), Expect = 53
Identities = 12/24 (50%), Positives = 15/24 (62%), Gaps = 8/24 (33%)

Query: 9 AFF-HQILA-TST-----IAMSH 24
AF HQ++A TST IAM+H
Sbjct: 148 AFLTHQVVAQTSTWIFKRSIAMNH 171

☐ >gi|17230565|ref|NP_487113.1| probable glycosyl transferase [Nostoc sp. PCC 7120
gi|25530026|pir|AB2190 hypothetical protein alr3073 [imported] - Nostoc sp. (str
7120)
gi|17132167|dbj|BAB74772.1| ORF_ID:alr3073~probable glycosyl transferase [Nostoc
Length = 324

Score = 26.1 bits (54), Expect = 53
Identities = 9/18 (50%), Positives = 9/18 (50%), Gaps = 8/18 (44%)

Query: 2 YKWPF---HFAPFHQIL 15
YKWPF HQIL
Sbjct: 185 YKWPFVVVKQ----HQIL 198

☐ >gi|27500354|ref|XP_211309.1| hypothetical protein XP_211309 [Homo sapiens]
Length = 132

Score = 26.1 bits (54), Expect = 53
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18
FHQIL+TS
Sbjct: 61 FHQILSTS 68

☐ >gi|13812138|ref|NP_113265.1| chromosomal region maintenance protein CRM1 [Guill
gi|25396709|pir|F90086 chromosomal region maintenance protein CRM1 [imported] -
theta nucleomorph
gi|13794450|gb|AAK39825.1|AF165818 33 chromosomal region maintenance protein CRM1
Length = 949

Score = 26.1 bits (54), Expect = 53
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 1/15 (6%)

Query: 10 FFHQILAT-STIAMS 23
FFH+IL STI MS
Sbjct: 358 FFHKILINLSTILMS 372

☐ >gi|27706584|ref|XP_242294.1| hypothetical protein XP_242294 [Rattus norvegicus]
Length = 415

Score = 26.1 bits (54), Expect = 53
Identities = 8/11 (72%), Positives = 10/11 (90%), Gaps = 1/11 (9%)

Query: 17 TSTIAMSHCRP 27
TS +AMS+CRP
Sbjct: 338 TS-VAMSNCRP 347

☐ >gi|100052|pir|S20988 lectin - garden pea
gi|169172|gb|AAA33691.1| vegetative lectin
Length = 265

Score = 26.1 bits (54), Expect = 53

Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 16 ATSTIAMSH 24
ATSTIA+SH
Sbjct: 235 ATSTIAVSH 243

☐ >[gi|7510844|pir|T29765](#) hypothetical protein ZC581.4 - *Caenorhabditis elegans*
Length = 209

Score = 26.1 bits (54), Expect = 53
Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 5 PFHF--AFFHQ--IL 15
PFHF FF Q IL
Sbjct: 57 PFHFPQTFFQPHIL 71

☐ >[gi|21398366|ref|NP_654351.1|A2012](#) hypothetical protein predicted by GeneMark [*Bacill*]
Length = 920

Score = 26.1 bits (54), Expect = 53
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 11 FHQILATS 18
FHQI+ATS
Sbjct: 439 FHQIMATS 446

☐ >[gi|5579428|gb|AAD45549.1|U70376_14](#) SpcE [*Streptomyces netropsis*]
Length = 427

Score = 26.1 bits (54), Expect = 53
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 3/15 (20%)

Query: 6 FH--FAFFHQ-ILAT 17
FH FAF HQ +LAT
Sbjct: 391 FHTCFAFLHQALLAT 405

☐ >[gi|630666|pir|S40748](#) hypothetical protein F54C8.6 - *Caenorhabditis elegans*
Length = 309

Score = 25.7 bits (53), Expect = 72
Identities = 11/22 (50%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 7 HFA--FFHQ----ILAT-STIA 21
HF FFHQ IL++ +TIA
Sbjct: 223 HFVVQFFHQIHLILSSIATIA 244

☐ >[gi|28917410|gb|EAA27114.1|](#) hypothetical protein [*Neurospora crassa*]
Length = 620

Score = 25.7 bits (53), Expect = 72
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 1 PYKWPFHF 8
PYKW F F
Sbjct: 36 PYKWTFQF 43

☐ >[gi|23612355|ref|NP_703935.1|](#) transportin [*Plasmodium falciparum* 3D7]
[gi|23498596|emb|CAD50547.1|](#) transportin [*Plasmodium falciparum* 3D7]
Length = 1147

Score = 25.7 bits (53), Expect = 72
Identities = 7/8 (87%), Positives = 7/8 (87%)

**results of BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053457234-04130-17010

search 2

Query=

(34 letters)

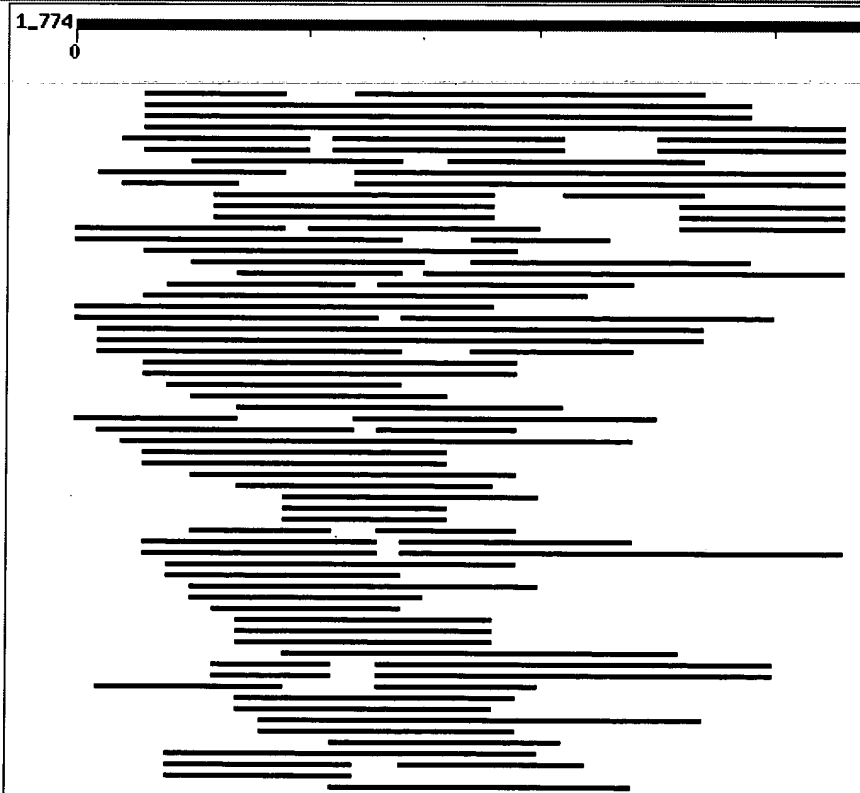
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

1,435,412 sequences; 461,393,641 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 101 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 20909630 ref XP_153478.1	hypothetical protein XP_153478...	30	3.8	L
gi 19113394 ref NP_596602.1	SNF2 family dna repair protein...	30	3.8	
gi 27685447 ref XP_217453.1	serine (or cysteine) proteinase...	29	5.1	L
gi 121111 sp P07092 GDN_RAT	Glia derived nexin precursor (G...	29	5.1	L
gi 21287767 gb EAA00088.1	ENSANGP00000017962 [Anopheles ga...	29	6.9	
gi 25148238 ref NP_499962.2	Protein kinase family member (...)	29	9.2	
gi 7505805 pir T34435	hypothetical protein K11H12.9 - Caen...	29	9.2	
gi 27695175 ref XP_223369.1	similar to low density lipopro...	28	12	L
gi 17558564 ref NP_506763.1	Predicted CDS, putative plasma...	28	12	L
gi 30145805 emb CAB02832.2	C. elegans SRW-24 protein (corr...	28	12	
gi 630666 pir S40748	hypothetical protein F54C8.6 - Caenor...	28	17	
gi 17555608 ref NP_498145.1	Predicted CDS, putative membra...	28	17	L
gi 17553568 ref NP_499077.1	Predicted CDS, putative membra...	28	17	L
gi 25342678 pir B88555	protein F54C8.6 [imported] - Caenor...	28	17	
gi 21245069 ref NP_644651.1	conserved hypothetical protein...	27	22	
gi 24374681 ref NP_718724.1	DnaJ domain protein [Shewanell...	27	30	
gi 10946860 ref NP_067441.1	TATA box binding protein (Tbp)...	27	30	L
gi 27672343 ref XP_221755.1	similar to hypothetical protei...	27	30	L
gi 28871387 ref NP_794006.1	hypothetical protein [Pseudomo...	27	30	
gi 20094540 ref NP_614387.1	Uncharacterized membrane prote...	27	30	
gi 9632199 ref NP_048911.1	a555R [Paramecium bursaria Chlo...	27	30	
gi 15078968 ref NP_149719.1	256R [Invertebrate iridescent ...]	27	40	
gi 30177923 gb EAA45104.1	ENSANGP00000023294 [Anopheles ga...	27	40	
gi 15641102 ref NP_230734.1	periplasmic binding protein-re...	27	40	
gi 19114288 ref NP_593376.1	hypothetical protein [Schizosa...	27	40	
gi 22293495 emb CAD31853.1	putative chemosensory receptor ...	26	54	
gi 17230565 ref NP_487113.1	probable glycosyl transferase ...	26	54	
gi 19552310 ref NP_600312.1	hypothetical membrane protein ...	26	54	
gi 22982800 ref ZP_00028030.1	hypothetical protein [Burkho...	26	54	
gi 14521448 ref NP_126924.1	CARBON STARVATION PROTEIN A. [...]	26	54	
gi 17544706 ref NP_501719.1	3-oxo-5-alpha-steroid 4-dehydr...	26	54	L
gi 7510844 pir T29765	hypothetical protein ZC581.4 - Caeno...	26	54	
gi 15235511 ref NP_195444.1	ATPase, E1-E2 type family [Ara...	26	54	
gi 5579428 gb AAD45549.1	U70376 14 SpcE [Streptomyces netro...	26	54	
gi 7710954 emb CAB90352.1	putative metal ATPase [Arabidops...	26	54	
gi 15606525 ref NP_213905.1	NADH dehydrogenase I chain M [...]	26	54	
gi 21242454 ref NP_642036.1	MFS transporter [Xanthomonas a...	26	72	
gi 28917410 gb EAA27114.1	hypothetical protein [Neurospora...	26	72	
gi 23612355 ref NP_703935.1	transportin [Plasmodium falcip...	26	72	
gi 17297993 dbj BAB78507.1	transportin [Plasmodium falcipa...	26	72	
gi 30177001 gb EAA08763.2	ENSANGP00000021306 [Anopheles ga...	26	72	
gi 27366492 ref NP_762019.1	Cation/multidrug efflux pump [...]	26	72	
gi 15903492 ref NP_359042.1	Conserved hypothetical protein...	26	72	
gi 13812138 ref NP_113265.1	chromosomal region maintenance...	26	72	
gi 13476001 ref NP_107571.1	ABC transporter, substrate bin...	26	72	
gi 30020491 ref NP_832122.1	hypothetical protein [Bacillus...	26	72	
gi 21244445 ref NP_644027.1	conserved hypothetical protein...	26	72	
gi 15226030 ref NP_179099.1	retroelement pol polyprotein -...	26	72	
gi 28901509 ref NP_801164.1	putative ferrichrome ABC trans...	26	72	
gi 15901437 ref NP_346041.1	conserved hypothetical protein...	26	72	
gi 23307111 dbj BAC16541.1	ferric vibrioferrin transport s...	26	72	
gi 30157001 ref XP_291865.2	similar to olfactory receptor ...	25	97	L
gi 17506261 ref NP_491002.1	Amino acid permease family mem...	25	97	L
gi 21224537 ref NP_630316.1	putative permease [Streptomyce...	25	97	
gi 30018841 ref NP_830472.1	Multidrug resistance protein B...	25	97	
gi 15611696 ref NP_223347.1	putative TYPE II DNA MODIFICAT...	25	97	
gi 15217347 gb AAK92685.1	AC090714 18 putative retrotranspo...	25	97	
gi 630612 pir S44629	F22B7.10 protein - Caenorhabditis ele...	25	97	
gi 16944534 emb CAD11330.1	hypothetical protein [Neurospor...	25	97	

gi 26251614 gb AAN84835.1	Hypothetical protein C55C2.5c [C...	25	97	
gi 1477386 gb AAC37338.1	This CDS feature is included to s...	25	97	
gi 24666563 ref NP_649079.2	CG6836-PA [Drosophila melanoga...	25	97	L
gi 17506263 ref NP_491003.1	Amino acid permease family mem...	25	97	L
gi 17861760 gb AAL39357.1	GH26215p [Drosophila melanogaster]	25	97	L
gi 17555266 ref NP_497282.1	Putative membrane protein, wit...	25	97	L
gi 26336525 dbj BAC31945.1	unnamed protein product [Mus mu...	25	97	L
gi 21231138 ref NP_637055.1	MFS transporter [Xanthomonas c...	25	97	
gi 30840221 emb CAD61285.1	fertility restorer [Raphanus sa...	25	97	
gi 17552842 ref NP_498909.1	DumPY : shorter than wild-type...	25	97	L
gi 21398624 ref NP_654609.1	sugar_tr, Sugar (and other) tr...	25	97	
gi 28564962 gb AAO32565.1	FKS1 [Saccharomyces kluyveri]	25	130	
gi 3914053 sp O13396 MSH2 NEUCR	DNA mismatch repair protein...	25	130	
gi 20837204 ref XP_158536.1	hypothetical protein XP_158536...	25	130	L
gi 29349732 ref NP_813235.1	conserved hypothetical protein...	25	130	
gi 23273294 gb AAH34950.1	TANK-binding kinase 1 [Homo sapi...	25	130	L
gi 19923703 ref NP_037056.2	CD44 antigen; Cell surface gly...	25	130	L
gi 7019547 ref NP_037386.1	TANK-binding kinase 1; NF-kB-ac...	25	130	L
gi 26991318 ref NP_746743.1	conserved hypothetical protein...	25	130	
gi 15791673 ref NP_281496.1	hypothetical protein Cj0305c [...	25	130	
gi 21595149 gb AAH32196.1	Unknown (protein for MGC:38244) ...	25	130	
gi 30022512 ref NP_834143.1	ABC transporter ATP-binding pr...	25	130	
gi 29377576 ref NP_816730.1	serine/threonine protein kinas...	25	130	
gi 27706584 ref XP_242294.1	hypothetical protein XP_242294...	25	130	L
gi 28521689 ref XP_288504.1	hypothetical protein XP_288504...	25	130	L
gi 22957373 gb ZP_00005078.1	hypothetical protein [Rhodoba...	25	130	
gi 17543364 ref NP_501353.1	Putative nuclear protein, with...	25	130	L
gi 21402483 ref NP_658468.1	ABC_tran, ABC transporter [Bac...	25	130	
gi 27368877 emb CAD59596.1	MRP-like ABC transporter [Oryza...	25	130	
gi 27718495 ref XP_216902.1	similar to TANK-binding kinase...	25	130	L
gi 21397994 ref NP_653979.1	hypothetical protein predicted...	24	174	
gi 15800733 ref NP_286747.1	unknown [Escherichia coli O157...	24	174	
gi 17456139 ref XP_051362.2	similar to Transmembrane 6 sup...	24	174	L
gi 84991 pir A20647	heat shock protein 22 - fruit fly (Dro...	24	174	L
gi 13473381 ref NP_104948.1	hypothetical protein [Mesorhiz...	24	174	
gi 17569347 ref NP_510111.1	Putative endoplasmic reticulum...	24	174	L
gi 27666390 ref XP_221376.1	similar to hypothetical protei...	24	174	L
gi 631889 pir C48213	syntaxin 2 - rat	24	174	
gi 27707330 ref XP_242328.1	hypothetical protein XP_242328...	24	174	L
gi 15830651 ref NP_309424.1	hypothetical protein [Escheric...	24	174	
gi 13124733 sp P02515 HS22 DROME	Heat shock protein 22	24	174	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|20909630|ref|XP_153478.1| hypothetical protein XP_153478 [Mus musculus]
Length = 197

Score = 29.9 bits (63), Expect = 3.8
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 4 WPFHFAF 10
WPFHFAF
Sbjct: 12 WPFHFAF 18

☐ >gi|19113394|ref|NP_596602.1| SNF2 family dna repair protein by similarity [Schi pombe]
gi|7492644|pir|T39936 probable helicase - fission yeast (Schizosaccharomyces pom

gi|3116120|emb|CAA18870.1| zinc finger protein; zf-C3HC4 type (RING finger); SNF2
 helicase; DEAD box helicase; putative DNA repair protein
 [Schizosaccharomyces pombe]
 Length = 1040

Score = 29.9 bits (63), Expect = 3.8
 Identities = 11/16 (68%), Positives = 12/16 (75%), Gaps = 1/16 (6%)

Query: 13 QILATIAMSHCRPTVY 28
 +IL IA SH RPTVY
 Sbjct: 458 EILTKIAPSH-RPTVY 472

☐ >gi|27685447|ref|XP_217453.1| serine (or cysteine) proteinase inhibitor, clade
 [Rattus norvegicus]
 Length = 398

Score = 29.5 bits (62), Expect = 5.1
 Identities = 12/27 (44%), Positives = 15/27 (55%), Gaps = 8/27 (29%)

Query: 4 WPFHFAFFHQILATIAMSHCRPTVYKQ 30
 W HF FF IL T+ +S +VY Q
 Sbjct: 3 W--HFPFF--ILTTVTLS----SVYSQ 21

☐ >gi|121111|sp|P07092|GDN RAT Glia derived nexin precursor (GDN) (Protease nexin
gi|92273|pir|B27496 proteinase inhibitor nexin 1 precursor - rat (fragment)
gi|204284|gb|AAA41209.1| GDN precursor
 Length = 397

Score = 29.5 bits (62), Expect = 5.1
 Identities = 12/27 (44%), Positives = 15/27 (55%), Gaps = 8/27 (29%)

Query: 4 WPFHFAFFHQILATIAMSHCRPTVYKQ 30
 W HF FF IL T+ +S +VY Q
 Sbjct: 3 W--HFPFF--ILTTVTLS----SVYSQ 21

☐ >gi|21287767|gb|EAA00088.1| ENSANGP00000017962 [Anopheles gambiae str. PEST]
 Length = 314

Score = 29.1 bits (61), Expect = 6.9
 Identities = 19/47 (40%), Positives = 22/47 (46%), Gaps = 20/47 (42%)

Query: 4 WPFHFAFFH---Q-----ILA--TI--AMSHCRPTVYKQTSII 34
 WP+H A FH Q IL TI A SHC VY Q+ +I
 Sbjct: 52 WPHVALFHRKDAQEYACGGSILDENTILTA-SHC---VYTQSGVI 94

☐ >gi|25148238|ref|NP_499962.2| Protein kinase family member (42.4 kD) [Caenorhabd
gi|17976530|gb|AAC24403.2| Hypothetical protein K11H12.9 [Caenorhabditis elegans]
 Length = 376

Score = 28.6 bits (60), Expect = 9.2
 Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 12 HQILATIAMSH 22
 HQILA +AM H
 Sbjct: 203 HQILAAVAMMH 213

☐ >gi|7505805|pir|T34435 hypothetical protein K11H12.9 - Caenorhabditis elegans
 Length = 374

Score = 28.6 bits (60), Expect = 9.2
 Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 12 HQILATIAMSH 22
 HQILA +AM H

Sbjct: 201 HQILAAVAMMH 211

☐ >[gi|27695175|ref|XP_223369.1|](#) similar to low density lipoprotein receptor-relat
low density lipoprotein-related protein 4; Low Density
Lipoprotein Receptor Related Protein 4; corin [Mus
musculus] [Rattus norvegicus]
Length = 276

Score = 28.2 bits (59), Expect = 12
Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 6 FHFAFFHQIL 15

FHF+ FHQ+L

Sbjct: 2 FHFSLFHQVL 11

☐ >[gi|17558564|ref|NP_506763.1|](#) Predicted CDS, putative plasma membrane membrane
member, with at least 5 transmembrane domains, nematode
specific [Caenorhabditis elegans]
[gi|7497294|pir|T19886](#) hypothetical protein C41G6.7 - Caenorhabditis elegans
Length = 405

Score = 28.2 bits (59), Expect = 12
Identities = 13/23 (56%), Positives = 15/23 (65%), Gaps = 4/23 (17%)

Query: 13 QILATIAMS-HCRPTVYKQTSII 34

IL +I MS HCR TV K SI+

Sbjct: 350 HILVSIMSSHCRDTV-K--SIV 369

☐ >[gi|30145805|emb|CAB02832.2|](#) C. elegans SRW-24 protein (corresponding sequence C
[Caenorhabditis elegans]
Length = 418

Score = 28.2 bits (59), Expect = 12
Identities = 13/23 (56%), Positives = 15/23 (65%), Gaps = 4/23 (17%)

Query: 13 QILATIAMS-HCRPTVYKQTSII 34

IL +I MS HCR TV K SI+

Sbjct: 363 HILVSIMSSHCRDTV-K--SIV 382

☐ >[gi|630666|pir|S40748](#) hypothetical protein F54C8.6 - Caenorhabditis elegans
Length = 309

Score = 27.8 bits (58), Expect = 17
Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19

HF FFHQI +ATIA

Sbjct: 223 HFVVQFFHQIHLILSSIATIA 244

☐ >[gi|17555608|ref|NP_498145.1|](#) Predicted CDS, putative membrane protein family m
least 4 transmembrane domains, nematode specific
[Caenorhabditis elegans]
[gi|7331800|gb|AAF60488.1|](#) Hypothetical protein Y32H12A.1 [Caenorhabditis elegans]
Length = 310

Score = 27.8 bits (58), Expect = 17
Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 11 FHQILATIAMS 21

FHQILA + MS

Sbjct: 47 FHQILAIVLMS 57

☐ >[gi|17553568|ref|NP_499077.1|](#) Predicted CDS, putative membrane protein, with a
domain, nematode specific [Caenorhabditis elegans]

gi|20141894|sp|P34444|YL86 CAEEL Hypothetical protein F54C8.6 in chromosome III
gi|15718117|emb|CAA80158.2| Hypothetical protein F54C8.6 [Caenorhabditis elegans]
 Length = 265

Score = 27.8 bits (58), Expect = 17
 Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19
 HF FFHQI +ATIA
 Sbjct: 223 HFVVQFFHQIIHLILSSIATIA 244

☐ >gi|25342678|pir|B88555 protein F54C8.6 [imported] - Caenorhabditis elegans
 Length = 306

Score = 27.8 bits (58), Expect = 17
 Identities = 11/22 (50%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 7 HFA--FFHQI-----LATIA 19
 HF FFHQI +ATIA
 Sbjct: 264 HFVVQFFHQIIHLILSSIATIA 285

☐ >gi|21245069|ref|NP_644651.1| conserved hypothetical protein [Xanthomonas axonop
 str. 306]
gi|21110802|gb|AAM39187.1| conserved hypothetical protein [Xanthomonas axonopodis
 str. 306]
 Length = 129

Score = 27.4 bits (57), Expect = 22
 Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 3 KWPFHFFAFF 11
 KW F FAFF
 Sbjct: 12 KWQFRFAFF 20

☐ >gi|24374681|ref|NP_718724.1| DnaJ domain protein [Shewanella oneidensis MR-1]
gi|24349326|gb|AAN56168.1|AE015754.2 DnaJ domain protein [Shewanella oneidensis M
 Length = 402

Score = 26.9 bits (56), Expect = 30
 Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 6 FHFAFFHQILA 16
 FH AFF QILA
 Sbjct: 170 FH-AFFEQILA 179

☐ >gi|10946860|ref|NP_067441.1| TATA box binding protein (Tbp)-associated factor,
 A [Mus musculus]
gi|1842204|emb|CAA71091.1| TAFI48 protein [Mus musculus]
 Length = 453

Score = 26.9 bits (56), Expect = 30
 Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFFAFF 11
 WP FHF+FF
 Sbjct: 380 WPAFHFSFF 388

☐ >gi|27672343|ref|XP_221755.1| similar to hypothetical protein MGC2408 [Homo sap
 norvegicus]
 Length = 256

Score = 26.9 bits (56), Expect = 30
 Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 2/16 (12%)

Query: 1 PYKWPF-HFAFFHQIL 15
 PY+W F FAFFH +L
 Sbjct: 130 PYEW-FGDFFAFFHALL 144

☐ >gi|28871387|ref|NP_794006.1| hypothetical protein [Pseudomonas syringae pv. tom
 gi|28854638|gb|AA057701.1| hypothetical protein [Pseudomonas syringae pv. tomato
 Length = 1111

Score = 26.9 bits (56), Expect = 30
 Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 FAFFHQIL 15
 FAFFHQ+L
 Sbjct: 728 FAFFHQLL 735

☐ >gi|20094540|ref|NP_614387.1| Uncharacterized membrane protein specific for M.ka
 family [Methanopyrus kandleri AV19]
 gi|19887659|gb|AAM02317.1| Uncharacterized membrane protein specific for M.kandle
 family [Methanopyrus kandleri AV19]
 Length = 244

Score = 26.9 bits (56), Expect = 30
 Identities = 10/22 (45%), Positives = 11/22 (50%), Gaps = 8/22 (36%)

Query: 4 WPFHFAFFHQILA-----TIAM 20
 W FAFF Q+L TI M
 Sbjct: 27 W---FAFFPQVLTFGLWLTIVM 45

☐ >gi|9632199|ref|NP_048911.1| a555R [Paramecium bursaria Chlorella virus 1]
 gi|7461690|pir|T18057 hypothetical protein a555R - Chlorella virus PBCV-1
 gi|2447141|gb|AAC96999.1| a555R [Paramecium bursaria Chlorella virus 1]
 Length = 113

Score = 26.9 bits (56), Expect = 30
 Identities = 10/16 (62%), Positives = 10/16 (62%), Gaps = 4/16 (25%)

Query: 14 ILATIA--MSHC--RP 25
 IL TI MSHC RP
 Sbjct: 60 ILETIVFIMSHCYKRP 75

☐ >gi|15078968|ref|NP_149719.1| 256R [Invertebrate iridescent virus 6]
 gi|15042337|gb|AAK82117.1|AF303741 256 256R [Chilo iridescent virus]
 Length = 78

Score = 26.5 bits (55), Expect = 40
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 YKWPFHFHAF 10
 ++W FHFHAF
 Sbjct: 39 FRWSFHFHAF 47

☐ >gi|30177923|gb|EAA45104.1| ENSANGP00000023294 [Anopheles gambiae str. PEST]
 Length = 232

Score = 26.5 bits (55), Expect = 40
 Identities = 15/36 (41%), Positives = 16/36 (44%), Gaps = 17/36 (47%)

Query: 4 WPFHFAFFHQ-----IL--ATI--AMSHC 23
 WP+H A FHQ IL TI A SHC
 Sbjct: 1 WPWHAAlFHQDKHKEYACGGSILDETTILTA-SHC 35

☐ >gi|15641102|ref|NP_230734.1| periplasmic binding protein-related protein [Vibri
 gi|11345643|pir|A82245 periplasmic binding protein-related protein VC1089 [impor
 Vibrio cholerae (strain N16961 serogroup O1)

gi|9655557|gb|AAF94248.1| periplasmic binding protein-related protein [Vibrio cho
Length = 270

Score = 26.5 bits (55), Expect = 40
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 5 PFHF AFFHQ 13

P+H+ FFHQ

Sbjct: 80 PYHYTFFHQ 88

☐ >gi|19114288|ref|NP_593376.1| hypothetical protein [Schizosaccharomyces pombe]
gi|3219957|sp|P87136|YDM5 SCHPO Hypothetical protein C57A7.05 in chromosome I
gi|7491179|pir|T38949 hypothetical protein SPAC57A7.05 - fission yeast
(Schizosaccharomyces pombe)
gi|2104440|emb|CAB08763.1| hypothetical protein; similar to S. cerevisiae YDL231C
contains 11 predicted transmembrane helices;
leucine-serine rich [Schizosaccharomyces pombe]
Length = 1337

Score = 26.5 bits (55), Expect = 40
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 3 KWPFHF 8

KWPFHF

Sbjct: 1308 KWPFHF 1313

☐ >gi|22293495|emb|CAD31853.1| putative chemosensory receptor 7 [Heliothis viresce
Length = 397

Score = 26.1 bits (54), Expect = 54
Identities = 10/17 (58%), Positives = 11/17 (64%), Gaps = 5/17 (29%)

Query: 1 PY--K-WPFHF AFFHQI 14

PY K WPF A+ HQI

Sbjct: 174 PYELKYWPF--AYIHQI 188

☐ >gi|17230565|ref|NP_487113.1| probable glycosyl transferase [Nostoc sp. PCC 7120
gi|25530026|pir|AB2190 hypothetical protein alr3073 [imported] - Nostoc sp. (str
7120)
gi|17132167|dbj|BAB74772.1| ORF_ID:alr3073-probable glycosyl transferase [Nostoc
Length = 324

Score = 26.1 bits (54), Expect = 54
Identities = 9/18 (50%), Positives = 9/18 (50%), Gaps = 8/18 (44%)

Query: 2 YKWPF---HFAFFHQIL 15

YKWPF HQIL

Sbjct: 185 YKWPFVVVKQ---HQIL 198

☐ >gi|19552310|ref|NP_600312.1| hypothetical membrane protein [Corynebacterium glu
13032]
gi|21323851|dbj|BAB98477.1| Hypothetical membrane protein [Corynebacterium glutam
13032]
Length = 241

Score = 26.1 bits (54), Expect = 54
Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 4/19 (21%)

Query: 4 WPFHF--AFFHQILATIAM 20

WPFHF A +I+A IA+

Sbjct: 71 WPFHFSDAL--RIIAAIAL 87

☐ >gi|22982800|ref|ZP_00028030.1| hypothetical protein [Burkholderia fungorum]
Length = 294

Score = 26.1 bits (54), Expect = 54
Identities = 10/16 (62%), Positives = 12/16 (75%), Gaps = 3/16 (18%)

Query: 13 QILATIAMSHCR--PT 26
+ILATI +HCR PT
Sbjct: 51 EILATI-RTHCRTVPT 65

☐ >gi|14521448|ref|NP_126924.1| CARBON STARVATION PROTEIN A. [Pyrococcus abyssi]
gi|7444677|pir|E75032 carbon starvation protein A homolog PAB1554 [similarity] -
Pyrococcus abyssi (strain Orsay)
gi|5458667|emb|CAB50154.1| cstA carbon starvation protein A [Pyrococcus abyssi]
Length = 592

Score = 26.1 bits (54), Expect = 54
Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 5/19 (26%)

Query: 4 WPFHFAF--FHQILATIAM 20
WP AF +Q+LA+IAM
Sbjct: 493 WP---AFSGMNQMLASIAM 508

☐ >gi|17544706|ref|NP_501719.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family memb
elegans]
gi|7510956|pir|T27720 hypothetical protein ZK1251.3 - Caenorhabditis elegans
gi|3881515|emb|CAA92499.1| Hypothetical protein ZK1251.3 [Caenorhabditis elegans]
Length = 253

Score = 26.1 bits (54), Expect = 54
Identities = 11/18 (61%), Positives = 11/18 (61%), Gaps = 5/18 (27%)

Query: 8 FAFFHQI---LATIAMSH 22
FAFF I LA AMSH
Sbjct: 214 FAFF--IVCNLAPRAMSH 229

☐ >gi|7510844|pir|T29765 hypothetical protein ZC581.4 - Caenorhabditis elegans
Length = 209

Score = 26.1 bits (54), Expect = 54
Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 5 PFHF--AFFHQ--IL 15
PFHF FF Q IL
Sbjct: 57 PFHFPQTFFQQPHIL 71

☐ >gi|15235511|ref|NP_195444.1| ATPase, E1-E2 type family [Arabidopsis thaliana]
gi|12643808|sp|Q9M3H5|AHM1 ARATH Potential cadmium/zinc-transporting ATPase HMA1
gi|25407802|pir|D85440 Cu2+-transporting ATPase-like protein [imported] - Arabid
thaliana
gi|4006855|emb|CAB16773.1| Cu2+-transporting ATPase-like protein [Arabidopsis tha
gi|7270710|emb|CAB80393.1| Cu2+-transporting ATPase-like protein [Arabidopsis tha
Length = 819

Score = 26.1 bits (54), Expect = 54
Identities = 11/27 (40%), Positives = 14/27 (51%), Gaps = 11/27 (40%)

Query: 2 YKWPFHFAFFHQILATIAMSHCRPTVY 28
+KWPF L+T A CR +VY
Sbjct: 385 FKWPF-----LSTAA---CRGSVY 400

☐ >gi|5579428|gb|AAD45549.1|U70376 14 SpcE [Streptomyces netropsis]
Length = 427

Score = 26.1 bits (54), Expect = 54
Identities = 10/15 (66%), Positives = 11/15 (73%), Gaps = 3/15 (20%)

Query: 6 FH--FAFFHQ-ILAT 17
 FH FAF HQ +LAT
 Sbjct: 391 FHTCFAFLHQALLAT 405

☐ >gi|7710954|emb|CAB90352.1| putative metal ATPase [Arabidopsis thaliana]
 Length = 819

Score = 26.1 bits (54), Expect = 54
 Identities = 11/27 (40%), Positives = 14/27 (51%), Gaps = 11/27 (40%)

Query: 2 YKWPFFHFAFFHQILATIAMSHCRPTVY 28
 +KWPF L+T A CR +VY
 Sbjct: 385 FKWPF-----LSTAA---CRGSVY 400

☐ >gi|15606525|ref|NP_213905.1| NADH dehydrogenase I chain M [Aquifex aeolicus]
 gi|7432313|pir|B70414 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoM
 Aquifex aeolicus
 gi|2983743|gb|AAC07304.1| NADH dehydrogenase I chain M [Aquifex aeolicus VF5]
 Length = 491

Score = 26.1 bits (54), Expect = 54
 Identities = 11/19 (57%), Positives = 12/19 (63%), Gaps = 3/19 (15%)

Query: 1 PYKWPFFHFAFFHQILATIA 19
 PY F FAFF +LA IA
 Sbjct: 370 PY---FTFAFFLAVLAGIA 385

Score = 19.7 bits (39), Expect = 4415
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 4 WPFH 7
 WPFH
 Sbjct: 226 WPFH 229

☐ >gi|21242454|ref|NP_642036.1| MFS transporter [Xanthomonas axonopodis pv. citri]
 gi|21107899|gb|AAM36572.1| MFS transporter [Xanthomonas axonopodis pv. citri str.
 Length = 474

Score = 25.7 bits (53), Expect = 72
 Identities = 10/17 (58%), Positives = 12/17 (70%), Gaps = 2/17 (11%)

Query: 6 FHFAFFHQILA--TIAM 20
 F FAFF Q LA T+A+
 Sbjct: 167 FAFAFFVQFLAVPTVAL 183

☐ >gi|28917410|gb|EAA27114.1| hypothetical protein [Neurospora crassa]
 Length = 620

Score = 25.7 bits (53), Expect = 72
 Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 1 PYKWPFFH 8
 PYKW F F
 Sbjct: 36 PYKWTFQF 43

☐ >gi|23612355|ref|NP_703935.1| transportin [Plasmodium falciparum 3D7]
 gi|23498596|emb|CAD50547.1| transportin [Plasmodium falciparum 3D7]
 Length = 1147

Score = 25.7 bits (53), Expect = 72
 Identities = 7/8 (87%), Positives = 7/8 (87%)